

STIC Database Tracking Number: 240590

To: BAO LI
Location: REM-3D24 / Mailbox 3C18
Art Unit: 1648
Thursday, October 18, 2007

Case Serial Number: 10/789355

From: TOBY PORT
Location: EIC 1600
REM-1D58 / REM-1A59
Phone: (571)272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner LI:

Enclosed are the results for the alignment portion of your sequence search. The results for Seq ID 30 translated and edited should be in SCORE on Monday. If you have any questions, please don't hesitate to call me.

Thank you for using STIC search services.

Toby Port
x22523

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2007, 17:20:08 ; Search time 5 Seconds
(without alignments)
36.902 Million cell updates/sec

Title: US-10-789-355A-30
Perfect score: 9605
Sequence: 1 gccagcccccagattgggggc.....ggcctctgcagatcaagt 9605

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 9605 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : aj238799.gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9605	100.0	9605	1	HCJ238799
2	33.4	0.3	9605	1	HCJ238799

ALIGNMENTS

RESULT 1
HCJ238799
LOCUS Hepatitis C virus type 1b complete genome, isolate Conl.
DEFINITION Hepatitis C virus type 1b complete genome, isolate Conl.
ACCESSION AJ238799
VERSION AJ238799.1 GI:5420376
KEYWORDS complete genome; core protein; glycoprotein E1; glycoprotein E2; NS2 proteinase/helicase; NS3/4A proteinase cofactor; NS4b protein; NS5A phosphoprotein; NS5B RNA dependant RNA polymerase; p7 peptide; polyprotein.
SOURCE Hepatitis C virus subtype 1b
ORGANISM Hepatitis C virus subtype 1b
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1
AUTHORS Lohmann, V., Korner, F., Koch, J., Herian, U., Theilmann, L. and Bartenschlager, R.
TITLE Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line
JOURNAL Science 285 (5424), 110-113 (1999)
PUBMED 10390360
REFERENCE 2 (bases 1 to 9605)
AUTHORS Bartenschlager, R.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-1999) Bartenschlager R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67,

FEATURES
source

55131 Mainz, GERMANY
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[illegible]

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RESULT 2

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DEFINITION
ACCESSION AJ238799
VERSION
KEYWORDS complete genome; NS3 proteinase/helicase; NS3/4A proteinase cofactor; NS4b protein; NS5A phosphoprotein; NS5B RNA dependant RNA polymerase; p7 peptide; polyprotein.
SOURCE Hepatitis C virus subtype 1b
ORGANISM Hepatitis C virus subtype 1b

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1
AUTHORS Lohmann, V., Korney, F., Koch, J., Herian, U., Theilmann, L. and Bartschlag, R.
TITLE Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line

JOURNAL Science 285 (5424), 110-113 (1999)

PUBMED 10390360

REFERENCE 2 (bases 1 to 9605)

AUTHORS Bartschlag, R.

TITLE Direct Submission

Submitted (10-MAY-1999) Bartschlag, R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67, 55131 Mainz, GERMANY

FEATURES

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Search completed: October 18, 2007, 17:20:14
Job time : 6 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 18, 2007, 17:16:54 ; Search time 9 Seconds
(without alignments)
4.698 Million cell updates/sec

Title: US-10-789-355A-30
Perfect score: 17788
Sequence: 1 gccagcccccgcattg9gggc.....ggcctctctgcagatcaagt 9605

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 1 seqs, 2201 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Database : seq4.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083-3-D2
; CURRENT APPLICATION NUMBER: US/10789,355A
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/257,857
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; PRIOR FILING DATE: 2001-12-21
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Db 1481 ArgProAspTyrAsnProLeu**GluSerTrpLysAspProAspTyrValProPro 1500
QY 7269 GTGTGTACAGCGGTGTCCATTGCGCTGCGCAAGGCCCTCCGATACACCTCCAGGAGG 7328
Db 1501 ValValHisGlyCysProLeuProProAlaLysAlaProProIleProProArgArg 1520
QY 7329 AAGAGGACGTTGTCTGTGTCAGATCTACCGTGTCTTCTCCCTTGGCGAGTCCGCCACA 7388
Db 1521 LysArgThrValValLeuSerGluSerThrValSerSerAlaLeuAlaGluLeuAlaThr 1540
QY 7389 AAGACCTTCGCGAGCTCCGAATCGTGGCGCTCGACAGCGGACCGCAACGCGCTCTCT 7448
Db 1541 LysThrPheGlySerSerGluSerSerAlaValAspSerGlyThrAlaThrAlaSerPro 1560
QY 7449 GACCGCCCTCCGAGCGGCGAGCGGATCCGACGTTGAGTGTGCTCTCCATCCGCTCC 7508
Db 1561 AspGlnProSerAspAspGlyAspAlaGlySerAspValGluSerTyrSerSerMetPro 1580
QY 7509 CCCCTTGGGGGAGCGCGGGATCCCGATCTCAGCGAGGGTCTTGGTCTTACCGTAAGC 7568
Db 1581 ProLeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrpSerThrValSer 1600
QY 7569 GAGGAGCTAGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7628
Db 1601 GluGluAlaSerGluAspValValCysCysSerMetSerTyrThrTrpThrGlyAlaLeu 1620
QY 7629 ATCAGCCCATGCTCGGAGGAAACCAAGCTGCCCATCAATGCTGCTGCTGCTGCTGCTG 7688
Db 1621 IleThrProCysAlaAlaGluGluThrLysLeuProIleAsnAlaLeuSerAsnSerLeu 1640
QY 7689 CTCCTGACCAACAATTTGGTCTATGTCACAACTCTCAGCGAGGGTCTTGGTCTTACCGTAAGC 7748
Db 1641 LeuArgHisHisAsnLeuValTyrAlaThrThrSerArgSerAlaSerLeuArgGlnLys 1660
QY 7749 AAGGTCACTTTTCACAGACTCGAGGTCTTGGACGACCACTACCGGAGCTGTCTCAAGGAG 7808
Db 1661 LysValThrPheAspArgLeuGlnValLeuAspAspHisTyrArgAspValLeuLysGlu 1680
QY 7809 ATGAGGCGAAGCGTCCAGTTAAGGCTAACTTCTATCCGTGAGGAGGAGCTGTAG 7868
Db 1681 MetLysAlaLysAlaSerThrValLysAlaLysLeuLeuSerValGluGluAlaCysLys 1700

Qy	7869	CTGAGCCCCCACAATTGCGGCAGATCTAAATTTGGCTATGGGCAAAAGGACGTCGCGAAC	7928
Db	1701	LeuThrProHisSerAlaAaGSerLysPheGlyTyrglyalalysaaspValaAaGAsn	1720
Qy	7929	CTATCCAGCAAGCCGTTAACCAATCCGCTCCGTTGGAGAGCACTTGCTGGAGAGACT	7988
Db	1721	LeuSerSerLysAlaValaAsnHisileAaGSerValTrpLysaaspLeuLeuGluAaspThr	1740
Qy	7989	GAGACACCAATTGACACCAATCATCGGCAAAATAATGAGGTTTTCTGCGTCCCAACAGAG	8048
Db	1741	GluThrProIleaspThrIleMetAlaLysAsnGluValPheCysValGlnProGlu	1760
Qy	8049	AAGGGGGCGCGCAAGCCAGCTCGCTTATCCGATATCCAGATTGGGGTTCGTGTGTC	8108
Db	1761	LysGlyGlyArgLysProAlaAaGLeuIleValPheProaspLeuGlyValAaGValCys	1780
Qy	8109	GAGAAATGCGCCTTACGATGTGCTCCACCTCCCTCAGCGCGTGATGGGCTCTTCA	8168
Db	1781	GluLysMetAlaLeuTyraaspValValSerThrLeuProGlnAlaValMetGlySerSer	1800
Qy	8169	TACGGATTCCAAATACTCTCTGGACACGGGTCGAGTTCTCTGCTGAATGCTCGAAAGCG	8228
Db	1801	TyrglyPheGlnTyserProGlyGluArgValGluPheLeuValaAsnAlaTrpLysAla	1820
Qy	8229	AAGAAATGCCCTATGGGCTTCGCATATGACACCCGCTGTTTGTACTCAACGGTCACTGAG	8288
Db	1821	LysLysCysProMetGlyPheAlaTyraThrArgCysPheaspSerThrValThrGlu	1840
Qy	8289	AATGACATCCGTGTGAGGAGTCAATCTACCAATGTTGTGACTTGGCCCCCGAAGCAGA	8348
Db	1841	AsnAspIleargValGluGluSerIleTyrgLncCysCysaspLeuAlaProGluAlaAaG	1860
Qy	8349	CAGGCCATAAGTCCGTCACAGAGCGCTTTACATCGGGGGCCCCCTGACTAATTTCTAAA	8408
Db	1861	GlnAlaIleargSerLeuThrGluArgLeuTyrgIleGlyGlyProleuThrAsnSerLys	1880
Qy	8409	GGGAGAACTCGCGCTATCGCCGGTCGGCGAGCGGTGTACTGACGACCCAGCTCGCGT	8468
Db	1881	GlyGlnAsnCysGlyTyraAaGArgCysAaGAlaSerGlyValLeuThrThrSerCysGly	1900
Qy	8469	AATACCTTCATGTTACTTGAAGCCGCTGCGGCCCTGTGAGCTGGGAAGCTCCAGGAC	8528
Db	1901	AsnThrLeuThrCysTyTrLeuLysAlaAlaAlaCysArgAlaLalLysLeuGlnAasp	1920
Qy	8529	TGCACGATGCTCGTATCGGAGACGACTTGTCGTTATCTGTGAAGCGCGGGACCCAA	8588
Db	1921	CysThrMetLeuValCysGlyAspAaspLeuValIleCysGluSerAlaGlyThrGln	1940
Qy	8589	GAGACAGAGCGAGCCTACCGGCCTTCACGGAGGCTATGACTAGATACTCTGCCCCCCCT	8648
Db	1941	GluaspGluAlaSerLeuAaGAlaPheThrGluAlaMetThrArgTyraSerAlaProPro	1960
Qy	8649	GGGAGCCGCCCAAACCAAGATACGACTTGGAGTTGATACATCATGCTCCTCCAAATGTG	8708
Db	1961	GlyAaspProProLysProCgluTyraaspLeuGluLeuIleThrSerCysSerSerAsnVal	1980
Qy	8709	TCAGTCGGCAGCATGCTCGGCAAAAGGGTGACTATCTCACCCCTGACCCCAACCAACC	8768
Db	1981	SerValAlaHisAaspAlaSerGlyLysAaGValTyrgLeuThrArgAaspProThrThr	2000
Qy	8769	CCCCCTGCGGGCTGCGTGGGACAGCTAGACACATCCAGTCAATTTCTGGCTAGGC	8828
Db	2001	ProLeuAlaAaGAlaAlaTrpGluThrAlaAaGHisThrProValaAsnSerTrpLeuGly	2020
Qy	8829	AACATCATGATGTATGCGCCCACTTGTGGGCAAGATGATCTCTGATGACTCATTTCTTC	8888
Db	2021	AsnIleIleMetTyraProThrLeuTrpAlaAaGMetIleLeuMetThrHisPhePhe	2040
Qy	8889	TCCATCTCTTAGCTCGAGAACACTTGAAAAGCCCTAGATTCTCAGATCTACGGGCCC	8948
Db	2041	SerIleLeuLeuAlaGlnGlnLeuGluLysAlaLeuaspCysGlnIleTyrglyAla	2060
Qy	8949	TGTTACTCCATGTAGCCACTTGACCTACTCAGATCATTTCAACGACTCCATGGGCTTAGC	9008

D	b		2061	CysTyrSerIleGluProLeuAspLeuprocinllelleglnargLeuHisGlyLeuSer	208
Q	y		9009	GCAVTTTCACATCCCATAGATTACTCTCCAGGTGAGATCAATAGGGTGCTTTCATGCCTCAGG	9068
D	b		2081	AlaPheSerLeuHisSerTySerProGlyGlulleasnArgValAlaSerCysLeuArg	2100
Q	y		9069	AACCTTGGGTACC CGCCTTCGAGTCTGGAGACATCGGCCAGAA GTGTCCGGCGCTAGG	9128
D	b		2101	LysLeuGlyValProProLeuArgValTrpArgHisArgAlaArgSerValArgAlaArg	2120
Q	y		9129	CTACTGTCCCAGGGGGGAGCGCTCCACTGTGTGGCAAGTA CTTCAA CTGCGCAGTA	9188
D	b		2121	LeuLeuSerGinGlyArgAlaAlaThrCysGlyLysTyLeuPheAsnTrpAlaVal	2140
Q	y		9189	AGGACCAAGCTCAA ACTCAC TCCA ATCCCC GCGCTCGTCCCA CAAGTTTGA TTATCCAGCTGG	9248
D	b		2141	ArgThrLysLeuLysLeuThrProIleProAlaAlaSerGinLeuAspLeuSerSerTrp	2160
Q	y		9249	TTCGTTGCTGTTTTACAGCGGGGAGACA TATA TCACAGCTGTCTCTGTGCCGACCCCGC	9308
D	b		2161	PheValAlaGlyTySerSrgLygAspiletyrHisSerLeuSerArgAlaArgProArg	2180
Q	y		9309	TGGTTTCATGTCGTGCTTACTTCTCTGTAGGGGTAGGCATCTATCTCTCTCCCCAAC	9368
D	b		2181	TrpPheMetTrpCysLeuLeuLeuSerValGlyValGlyIleTyLeuLeuProAsn	2200
Q	y		9369	CGA 9371 	
D	b		2201	Arg 2201	
RESULT 2					
US-10-789-355A-4					
; Sequence 4, Application US/10789355A					
; GENERAL INFORMATION:					
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.					
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM					
; FILE REFERENCE: HEPATITIS C VIRUS					
; CURRENT APPLICATION NUMBER: US/10789,355A					
; PRIOR FILING DATE: 2004-02-27					
; PRIOR FILING DATE: 2000-12-22					
; PRIOR FILING DATE: 2001-12-21					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 4					
; LENGTH: 2201					
; TYPE: PRT					
; ORGANISM: HCV					
; FEATURE:					
; NAME/KEY: VARIANT					
; LOCATION: 882					
; OTHER INFORMATION: Xaa is Lys or Arg					
; FEATURE:					
; NAME/KEY: VARIANT					
; LOCATION: 1489					
; OTHER INFORMATION: Xaa is Leu					
US-10-789-355A-4					
Alignment Scores:					
Pred. No.: 0 Length: 2201					
Score: 131.50 Matches: 423					
Percent Similarity: 28.6% Conservative: 208					
Best Local Similarity: 19.2% Mismatches: 726					
Query Match: 0.7% Indels: 855					
DB: 1 Gaps: 101					
US-10-789-355A-30 (1-9605) x US-10-789-355A-4 (1-2201)					
Q	y		8815	TTGACTGGAGTGTGTACTCTCTCCACGACGCCCGCGAGGGGGTGTGGGTCA	8750
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Db 265 ValAsnGlyValCysTrpThrValThrHisGlyAlaGlySerLysThrLeuAlaGlyPro 284
 QY 8755 CGG-----GTGAGATGATACAC----- 8738
 Db 285 LysGlyProIleThrGlnMetThrThrAsnValAspGlnAspLeuValGlyTrpGlnAla 304
 QY 8737 ---CTTTGGCAGATGATCGTGGCGGACGACACATG----- 8702
 Db 305 ProProGlyAlaArgSerLeuThrProCysThrCysGlySerAspLeuThrLeuVal 324
 QY 8701 --GAGGAGCATGATGTTATC----- 8684
 Db 325 ThrArgHisAlaAspValIleProValArgArgGlyAspSerArgGlySerLeuLeu 344
 QY 8683 AACTCCAAAGTCGATTTCTGTTTGGCGGTCCTCCAGCGGGG----- 8642
 Db 345 SerProArgProValSerThrLeuLysGlySerSerGlyGlyProLeuLeuCysProSer 364
 QY 8641 -----GCAGAGTATCTAGTCATAGCTCCGTAAGGCCCGTAGGTCGCTCGTCC----- 8591
 Db 365 GlyHisAlaValGlyIlePheArgAlaAlaValCysThrArgGlyValAlaLysAlaVal 384
 QY 8590 TCTTGGTCCCGCGCTTTCACAGATAACGACAGGTCTCTCCGCA-TACGAGCATCGT 8532
 Db 385 AspPheValProValGluSerMetGluThrThrMetArgSerProValPheThrAspAsn 404
 QY 8531 GCA-----GTCCTGGAGCTTCGACGCTCGACAGGC 8502
 Db 405 SerSerProProAlaValProGlnThrPheGlnValAlaHisLeuHisAlaProThrGly 424
 QY 8501 CGCAGCGCCTTCAAGTAACATGTGAGGTATACCGCAGCTGGTGTGTCAGTACACCGT 8442
 Db 425 --SerGlyLysSerThrLysValProAlaAlaThrAlaAlaGlnGlyTrpLysValLeu 443
 QY 8441 CGCGCGGCACCGGCATAGCCAGTCTGCCCTTTAGAAATAGTCAGGGGGC----- 8388
 Db 444 ValLeuAsnProSerValAlaAlaThrLeuGlyPhe-----GlyAlaTrpMet 459
 QY 8387 -----CCCGATGATAAG----- 8376
 Db 460 SerLysAlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIleThrThrGly 479
 QY 8375 ---CGCTCTGTGACGACCTTATGCG-----CTGTCTGGCTTCGGGGCCCAAGTCACAACA 8322
 Db 480 AlaProIleThrThrSerThrThrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGly 499
 QY 8321 TTGTGATGATGCTCTCAA-CACGATGTCTATCTCAGTGACCGTTGAGTCAAAACAGC 8263
 Db 500 AlaTrpAspIleIleCysAspGluCysHisSer----- 511
 QY 8262 GGGTGTATATGCGAAGCCATAGGCGATTTCTGCTTTCCAGGCAATTCACAGGAAT 8203
 Db 512 -----ThrAspSerThrThrIleLeuGlyIleGlyThr 522
 QY 8202 CGACCGCTGTCCAGGAGATATTGGAATCCGTATG-----AAGACCCCATCAGCGCT 8149
 Db 523 ValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrPro 542
 QY 8148 GAGGAGGGTGGAGA---CCACAT-----CGTAAAGGCCATTTTCTCGCACACAC 8101
 Db 543 ProGlySerValThrValProHisProAsnIleGluValAlaLeuSerSerThrGly 562
 QY 8100 GAACCCCAATCTGGATACGATAAGCGAGCTGGCTTGGCGGCCCCCTCTCTGTT 8041
 Db 563 GluIleProPheThrGly-----LysAlaIleProIleGluThrIleLys 577
 QY 8040 GGACGACAGAACCTCATTTTGGCATGAT----- 8010
 Db 578 GlyGlyArg-HisLeuIlePheCysHisSerLysLysCysAspGluLeuAlaLys 597
 QY 8009 -----GGTGGTGTCAATTGGTGTCTCAGTGTCTTCCAGCAAGTCTCT 7969
 Db 597 sLeuSerGlyLeuGlyLeuAsnAlaValAlaTrpThrArgGlyLeuAspValSerValIle 617

QY 7968 TCACACGAGCGAGCGATGTGGTTAAACGGCCTTGCTGTGATAGTTCCGAGCGTCTTTGGCCC 7909
 Db 617 eProThrSerGlyAspValIle-----ValValAla 628
 QY 7908 CATAGCCAAATTTAGATCTGGCCGAATGTGGGGCGTCAGCTTACAGGCTTCTCCACCG 7849
 Db 628 rAspAla-----LeuMetThrGlyPhe----- 635
 QY 7848 ATAGAAGTTTAGCCTTAACTGTGGACGCTTCCGCTTCATCTCTTGGACGACGTCGCGT 7789
 Db 635 ----- 635
 QY 7788 AGTGGTGTCCAGGACCTGCAGTGTGCAAGGTGACCTTCTTCTCGCGAGGCTTGGCG 7729
 Db 636 -----ThrGlyAsp----- 638
 QY 7728 TGCAGATGTTGTAGCATAGACCAAGTTGTGGTGACGGAGCAAGAGTTGCTCAGTGCAT 7669
 Db 639 -----PheAspSerValIleAspCysAsnThrCysValThrGlnThrVa 653
 QY 7668 TGATGGCAGCTTGGTTTCTCCGACGCGATGGCGTGATCAGGGCGCTTCCATGTGT 7609
 Db 653 lAspPheSerLeu----- 657
 QY 7608 AGGACATCGAGCAGCAGACGCTCTCACTAGCCTCTCGTCTTACGGTAGACCAAGACC 7549
 Db 658 -----AspProThrPheThr-IleGluThrThrThrValProGlnAspA 672
 QY 7548 CGTGGTGTAGATCGGATCCCGCGTCCCTCAAGGGGGCGCATGGAGGATGACACT 7489
 Db 672 laValSerArgSerGlnArgGlyArgThrGlyArgGlyIleThrArgP 692
 QY 7488 CAACGTCGATCCCGCTCGCGTCTCGAGGGCTGTCAGGAGGGCGTTCGCGTGC 7429
 Db 692 heValThrProGlyGluArgProSer-----GlyMetPheAspSerSerValLeu-Cys 709
 QY 7428 CGCTGT----- 7423
 Db 710 GluCysTrpAspAlaGlyCysAlaTrpTyThrGluLeuThrProAlaGluThrSerValArg 729
 QY 7422 -----CGAGCGCGCAGATTCGGAGCTCGCAAGGCTTTG-----TGG 7384
 Db 730 LeuArgAlaTrpLeuAsnThrProGlyLeuProValCysGlnAspHisLeuGluPheTrp 749
 QY 7383 CGAGCTCCGCCAAGGACAGACACGCTAGATTCTCAGCAGGACACCGTCC----- 7333
 Db 750 GluSer-----ValPheThrGlyLeuThrHisIleAspAla 761
 QY 7332 -----TCTTCTCCGTGGAGTGGTATCGAGGGCGCTTGGCAGCGCGCAATGGAC 7282
 Db 762 HisPheLeuSerGlnThrLysGlnAlaGlyAspAsnPheProTrpLeuValAlaTrpGln 781
 QY 7281 ACCGTGTACACTGGAGGACGATGTCGGGTCCTTCCAGGACTTAACAGTGGAGGT 7222
 Db 782 AlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGln-MetTrpLysC 801
 QY 7221 TGTAACTCCGGGTGCCATATGGGCATCGCTCGAGGAAATTCCTGGACCTCCGACGGA 7162
 Db 801 sLeuIleArgLeuLysProThrLeuHis-----GlyProThr----- 813
 QY 7161 TCTCCCGCGGACGGATACTTCCCTCTCATCTCTCCCTCGCTTGGAGCGCTGAAAGAT 7102
 Db 814 -----ProLeu-----LeuTrpArgLeuGlyAlaVa 822
 QY 7101 CCAAAATTACTACCTTATTTTCTGACTCCACGCGGTGTATGTTCCCGCCCATCTCTGCC 7042
 Db 822 lGlnAsnGluValThr-----ThrHisProIleThrLysTrpIleMetal 838
 QY 7041 GCCACAGGAGGTGGCTCGATGAGGTCCAGCGTCCGGGAGTCAATCAGCGGT----- 6990
 Db 838 aCysMetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValle 858

Db 1416 -----AspLeuIleGluAlaAsnLeuLeu 1423
Qy 5065 TGGGA-CAAGAAATGGCGTCTATGTGGGTGAG-----GCTGT 5028
Db 1424 TrpArgGlnGluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIle 1443
Qy 5027 AAAGACGCTCTCCAGAACTCCAGATGGT-CTGGCAGACGGCAACCTCGTGTGTTA 4969
Db 1444 LeuAspSerPheGluProLeuGlnAlaGluGluAspGluArgGluValSerVal-----1461
Qy 4968 GGTAAAGCCCGCAACCTAACTAGGTCTCGCGGGCGTGAGTGTACCAAGCACAGCCCG 4909
Db 1462 -----ProAlaGluIleuArg-----1467
Qy 4908 CGTCATAGCACTCGCACAAACCGAGGAATCGAATCGCCGAGGGCGGTTCTCTCGAG 4849
Db 1468 -----ArgSerArgLysPheProArgAlaMetProIleTyr 1479
Qy 4848 TCA-----CAAACCTGTAATGCCCA-----4828
Db 1480 AlaArgProAspTyrAsnProLeu**GluSerTrpLysAspProAspTyrValPro 1499
Qy 4827 -----TCCTGCGCCCTACCAGTCTCGCTCGCGCTCGAGCGTGACACCGCGT 4780
Db 1500 ProValValHisGlyCysProLeuProProAlaLysAlaProProIleProProArg 1519
Qy 4779 CTTGT-GGCACGCTCGTCTCAATGTGTGAAGTCTCGAGTCCAGGTGAGTCTGCTC 4721
Db 1520 ArgLysArgThrValValLeuSerGluSerThrValSerSerAlaLeuAlaGluLeuAla 1539
Qy 4720 TGGGTGACA-----CATGTATTCAGTCTGATCACTAGTACGTAATCG 4679
Db 1540 ThrLysThrPheGlySerSerGluSerSerAlaValAspSerGlyThrAlaThrAlaSer 1559
Qy 4678 CCGGTAAAGCCC-----4667
Db 1560 ProAspGlnProSerAspGlyAspAlaGlySerAspValGluSerTyrSerMet 1579
Qy 4667 -----4667
Db 1580 ProProLeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrpSerThrVal 1599
Qy 4666 -----GTCATTAGAGCGTCCGTTGTCTACGACAAATGACGTCTCCG 4628
Db 1600 SerGluGluAlaSerGluAspValValCysCysSerMetSerTyrThrTrpThrGlyAla 1619
Qy 4627 CTAGTTGT-----ATGACGATAC-ATCAGGCCCGCCGTA-----4593
Db 1620 LeuIleThrProCysAlaAlaGluGluThrLysLeuProIleAsnAlaLeuSerAsnSer 1639
Qy 4592 -----ATATGCTACAGCATTTGAGTCTCGAGCGCGACAGTCTCGCGC 4551
Db 1640 LeuLeuArgHisHisAsnLeuValYrAlaThrThrSerArgSerAlaSerLeuArgGln 1659
Qy 4550 GAGCTCATCATATTT-----4536
Db 1660 LysLysValThrPheAspArgLeuGlnValLeuAspHisTyrArgAspValLeuLys 1679
Qy 4535 -----CTTCTGGAATGGCAGAAAT---4515
Db 1680 GluMetLysAlaLysAlaSerThrValLysAlaLysLeuLeuSerValGluGluAlaCys 1699
Qy 4514 GAGGTGCTCCCGCTTCGATGGTCTCGATGGGATGGCTTTCCATAAAGG-----4461
Db 1700 LysLeuThrProProHisSerAlaArgSerLysPheGlyTyrGlyAlaLysAspValArg 1719
Qy 4460 GATTCTCCAGTCTCGACAGACCACTCTCCGATGTTGTGATGTGGCAGCGTACCGA 4401
Db 1720 AsnLeuSerSerLysAlaValAsnHisIleArgSerValTrp-----1733
Qy 4400 TCCCGAGCGGTAGCGGTGGCAGCAGCAGTCCGCTCCAGCGCTCTCGCTGTGTC 4341
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Qy 4340 CAGGAC-----TGTGCCGATGCCAGGATAGTGGTCTCAGTCAGTTGAGTGGCAGCTC 4290
Db 1751 LysAsnGluValPheCysValGlnProGluLysGlyArgLysPro---AlaArgLeu 1769
Qy 4289 ATCACATAT-----TATGATGTCATA 4269
Db 1770 IleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeuTyrAspValVal 1789
Qy 4268 GGGCGCCCGCAGAGCAACACCGCTCGC-----4242
Db 1790 SerThrLeuProGlnAlaValMetGlySerSerTyrGlyPheGlnTyrSerProGlyGln 1809
Qy 4241 -----AGAAACTTGCATAGTGGAGTACGT 4215
Db 1810 ArgValGluPheLeuValAsnAlaTrpLysAlaLysLysCysProMetGlyPheAlaTyr 1829
Qy 4214 GATGGGGCACCGCT---GGTGTGTCTTATCCCGGTTCTGATGTAGGTGCGATACC 4158
Db 1830 Asp-----ThrArgCysPheAspSerThrValThrGluAsnAspIleArgValGluGlu 1847
Qy 4157 -----ATGTGCTTATAGCATATACGCCCGAAACCTAGGTGTGGCGCGCAGGAC-- 4109
Db 1848 SerIleTyrGlnCys-CysAspLeu---AlaProGluAlaArgGlnAlaIleArgSerLe 1866
Qy 4108 -----GGTT 4104
Db 1866 uThrGluArgLeuTyrIleGlyGlyProLeuThrAsnSerLysGlyGlnAsnCysGlyTy 1886
Qy 4103 CAGGACAGCACCTTATACCTTGGGTGCTGATAGCGAGCGGC---ACCTAGTGTCTT 4047
Db 1886 rArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCysTy 1906
Qy 4046 GCCGTACCACTAGTAGGCGGTAGATGGGCACCTGGAATGCTCTGGTACCGCGCGAGG 3987
Db 1906 rLeuLysAlaAlaAlaCysArgAlaLysLeuGlnAspCys-----1921
Qy 3986 GGCAGGATTTGCTCGTGAAGACCGGGGACCGCATAGTGTGTTCATAGCTCGACGGGTAC 3927
Db 1922 -----ThrMetLeuValCysGlyAspLeuValValIleCysGluSerAlaGlyTh 1939
Qy 3926 AAGTCCACCGCTTGCACACCTCGGTGTCACACGCGAGCGCGGAAGATGCCACAGC 3867
Db 1939 rGlnGluAspGlu---AlaSerLeuArgAlaPheThrGluAlaMetThr-----1954
Qy 3866 GTCCCCCGGCGGACAGACGAGTGCACCGCCGGAAGACCTTCAAGTAGGAGACGGCCT 3807
Db 1955 -----ArgTyrSerAlaProProGlyAspProProLysProGluTyrAspLe 1970
Qy 3806 GGGGAGAGTAGTCTCCCTGCTGCTCGCCCGCGCGCACCGGAATGATCGCATG 3747
Db 1970 uGlu-----1971
Qy 3746 CTTCTGTGACCAAGTAAGTTCGAGTGCAGCGAGTGCATGTGTCAAGGACCGCGCCC 3687
Db 1972 -LeuIleThrSerCysSerSerAsnValSerValAlaHisAspAlaSerGlyLysArg-- 1990
Qy 3686 GGGGGCGCTTGGCCAGCGGACAGTCTCTGTCACATTTGTTGTGCGTGGAGACCACTTGG 3627
Db 1991 -----ValTyrLeuThrArgAs 1997
Qy 3626 GCCCTTTGGGCGC---GCAAGGTCTTTGAGCGCGCACCATGATAGACAGTCCCAACACAC 3570
Db 1997 pProThrThrProLeuAlaArg-----AlaAlaTrpGluThrAlaArgHisTh 2013
Qy 3569 GCCATTGACGAGGTGCGCCAGGAAGATTGTGTGCGGTGGAGACCACTTGGACC-----3515
Db 2013 rProVal-----AsnSerTrpLeuGlyAs 2021
Qy 3514 -----TCCCGCTCGACCTGTTCTCTGTCGCCGCTGTGGCGCTGTAGGTATGAT 3468
Db 2021 nIleIleMetTyrAlaProThrLeuTrp-----AlaArgMetIleLeuMe 2036

Qy 3467 G 3467
Db 2036 t 2036

Search completed: October 18, 2007, 17:17:24
Job time : 24.5 secs

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4250 4260 4270 4280 4290 4300 4310 4320
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4250 4260 4270 4280 4290 4300 4310 4320
4330 4340 4350 4360 4370 4380 4390
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4400 4410 4420 4430 4440 4450 4460
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4470 4480 4490 4500 4510 4520 4530
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[illegible]


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6820 6830 6840 6850 6860 6870 6880
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6890 6900 6910 6920 6930 6940 6950
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7030 7040 7050 7060 7070 7080 7090
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7180 7190 7200 7210 7220 7230 7240
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7250 7260 7270 7280 7290 7300 7310
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7320 7330 7340 7350 7360 7370 7380
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7390 7400 7410 7420 7430 7440 7450
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[illegible]

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